

IN THE CLAIMS:

Please amend claims 1-4 and 30-37 as follows:

1. (Currently Amended) A primer design system, comprising:
 - means for selecting at least one genomic DNA nucleotide sequence from a database including a plurality of genomic DNA nucleotide sequences;
 - means for predicting a plurality of exons of said selected DNA nucleotide and for storing positions of the predicted exons;
 - means for designing corresponding primer pairs for each of the predicted exons simultaneously by using each of the predicted exons as a template to design one corresponding primer pair for each of the predicted exons ~~and for designing corresponding primer pairs for the predicted exons simultaneously~~; and
 - means for automatically collating said plurality of primer pairs with said predicted exons and the DNA nucleotide sequence.
2. (Currently Amended) ~~[[A]]~~The primer design system according to claim 1, further comprising means for selecting a plurality of primer pairs meeting certain selection conditions from the designed primer pairs.
3. (Currently Amended) ~~[[A]]~~The primer design system according to claim 2, wherein said selection conditions include at least one of a predetermined base length, a range of GC content and a range of melting temperature T_m.
4. (Currently Amended) ~~[[A]]~~The primer design system according to claim 1, further comprising means for evaluating specificity of each ~~designed~~ primer ~~or~~ of designed primer pairs by a sequence alignment program.
- 5-29. (Cancelled)
30. (Currently Amended) A method for designing primers, comprising the steps of:
 - selecting at least one genomic DNA nucleotide sequence from a genomic DNA database;

predicting a plurality of exons of said selected DNA nucleotide;
designing corresponding primer pairs for the predicted exons simultaneously by
 using each of the predicted exons as a template to design one corresponding primer pair
 for each of the predicted exons ~~and for designing corresponding primer pairs for the~~
~~predicted exons simultaneously~~; and
 automatically collating said plurality of primer pairs with said predicted exons and
 the DNA nucleotide sequence.

31. (Currently Amended) [[A]]The method for designing primers according to claim 30,
 further comprising a step of selecting a plurality of primer pairs meeting certain selection
 conditions from said plurality of designed primer pairs, wherein said ~~extraction~~ selection
 conditions include at least one of a predetermined base length, a GC content, a range of
melting temperature T_m.
32. (Currently Amended) [[A]]The method for designing primers according to claim 30,
 further comprising a step of evaluating specificity of each ~~designed primer~~ or of designed
primer pairs.
33. (Currently Amended) [[A]]The primer design system according to claim 1, further
 comprising means for randomly dividing fragments of a genomic DNA [[as]] into
 templates for exon prediction.
34. (Currently Amended) A primer design system, comprising:
 - means for selecting at least one genomic DNA nucleotide sequence from a
 database including a plurality of genomic DNA nucleotide sequences;
 - means for predicting a plurality of exons of said selected DNA nucleotide and for
 storing positions of the predicted exons;
 - means for designing corresponding primer pairs for the predicted exons
simultaneously by using each of the predicted exons as a template to design one
 corresponding primer pair for each of the predicted exons ~~and for designing~~
~~corresponding primer pairs for the predicted exons simultaneously~~; and
 - means for evaluating specificity of each ~~designed primer~~ or each of designed

primer pairs.

35. (Currently Amended) ~~[[A]]~~The primer design system according to claim 34, wherein the ~~means for~~ system is capable of evaluating ~~specificity~~evaluates each designed primer by conducting homology searches for a full sequence of the primer via at least one repeat database and at least one genome database.
36. (Currently Amended) ~~[[A]]~~The primer design system according to claim 34, wherein the ~~means for~~ system is capable of evaluating ~~specificity~~evaluates each designed primer by conducting a homology search for any undesirable sequence contained therein.
37. (Currently Amended) ~~[[A]]~~The primer design system according to claim 34, wherein the ~~means for~~ system is capable of evaluating ~~specificity~~evaluates each designed primer pair by conducting ~~justification~~ specificity checks on ~~each multiplication~~ an amplification region in the DNA which contains an exact sequence as the primer but positioned elsewhere ~~[[on]]~~in the DNA.